

File Copy
09/466778
STW

=> d his

(FILE 'HOME' ENTERED AT 13:15:51 ON 15 APR 2001)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, SCISEARCH' ENTERED AT 13:16:36 ON
15 APR 2001

L1	3 S FELL PROTEIN
L2	388 S HYALURONATE (P) (BINDING (W) PROTEIN)
L3	584 S L2 OR HABP
L4	0 S L3 (P) FELL
L5	0 S L3 AND L1
L6	30 S L3 (P) CD44
L7	0 S L3 (P) ((CD44 (S) PRECURSOR))
L8	0 S L3 (P) ((CD44 (W) LIKE))

=> log off y

09/466778

File Copy
EAST
Search Strategy

Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
1	BRS L1	0	FELL adj protein	USPA T; US-P GPUB ; EPO; JPO; DERW ENT	2001/04/1 5 12:31			0
2	BRS L7	23	CD44 same precursor	USPA T; US-P GPUB ; EPO; JPO; DERW ENT	2001/04/1 5 12:38			0
3	BRS L19	2	L13 same CD44	USPA T; US-P GPUB ; EPO; JPO; DERW ENT	2001/04/1 5 12:41			0
4	BRS L13	16	hyaluronate with (binding adj protein)	USPA T; US-P GPUB ; EPO; JPO; DERW ENT	2001/04/1 5 12:50			0

	Type	L #	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors
5	BRS	L25	26	L13 or HABP	USPA T; US-P GPUB ; EPO; JPO; DERW ENT	2001/04/15 12:51			0

(85)

**National Center for Biotechnology Information**

National Library of Medicine

National Institutes of Health

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

Search for **SITE MAP**

About NCBI
general and
contact
information

GenBank
sequence
submission
support and
software

Molecular
databases
sequences,
structures and
taxonomy

Literature
databases
PubMed and
OMIM

Genomic
biology
the human
genome, whole
genomes and
related
resources

Tools
for data mining

Research at
NCBI
people, projects
and seminars

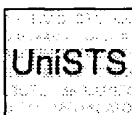
Education

What does NCBI do?

Established in 1988 as a national resource for molecular biology information, NCBI creates public databases, conducts research in computational biology, develops software tools for analyzing genome data, and disseminates biomedical information - all for the better understanding of molecular processes affecting human health and disease.

Draft Human Genome

Explore [human genome resources](#) or browse the human genome sequence using the [Map Viewer](#).

Integrated STS reports

UniSTS presents marker information collected from public resources including GenBank, RHdb, GDB, and various maps. Zero in on primer and mapping data, e-PCR results, and Map Viewer and LocusLink cross-references. More...

[Archives](#)**NCBI in the News**

The draft sequences of the human genome were compared in an article by Aach et al. (*Nature*, Feb.

Hot Spots

➤ Cancer
genome
anatomy project

➤ Clusters of
orthologous
groups

➤ Coffee Break

➤ Electronic
PCR

➤ Gene
expression
omnibus

➤ Genes and
disease

➤ Human
genome
resources

➤ Human/mouse
homology maps

➤ LocusLink

➤ Malaria
genetics &
genomics

➤ ORF finder

➤ Reference
sequence
project

➤

teaching
resources and
on-line tutorials

FTP site
download data
and software

15), noting overall similarities but differences in details. Use of RefSeq, NCBI's manually curated database of mRNA sequences, is credited with providing additional gene annotation for the public sequence.

[Disclaimer](#) [Privacy statement](#)

Revised April 4, 2001

Retrovirus
resources

➤ Serial analysis
of gene
expression

➤ Trace archive

➤ UniGene

➤ VecScreen

85

GeneCards is copyright. Usage by and for commercial entities requires a license agreement.



GeneCards: human genes, maps, proteins and diseases

GeneCards is a database of human genes, their products and their involvement in diseases. It offers **concise information** about the **functions** of all **human genes** that have an approved symbol, as well as selected others [[gene listing](#)].

Credits

Mirror sites

Jobs

About GeneCards

[Disease genes](#)

[How to Mirror](#)

[Guiding the user](#)

[Data Sources](#)

[Data Extraction](#)

[Usage statistics](#)

[Citing this resource](#)

[Publications](#)

What's New

Version: 2.19
Release: Jan 31, 2001
Entries: 18,583
Approved*: 11,980

About Bioinformatics

[Data Mining in](#)

[Biology](#)

[Web Usability](#)

[Science on the Web](#)

Your Feedback

GeneCards now also supports searching **UDB** (The Unified Database for Human Genome Mapping). [Read more about UDB.](#)

Search

[[Quick Start](#)] [[Guided Tour](#)] [[More search examples](#)]

- Search/Display GeneCards by

*For example, you can display the GeneCard for the (case-sensitive) symbol **BRCA1**.*

or search GeneCards for the keyword(s):

- o [p53](#)
- o [apolipoprot*AND \(hyper* OR Alzheimer*\)](#)
- o [U85267](#) *GenBank accession No.*
- o [Hs.1288](#) *UniGene cluster*
- o [ATCC:106253](#), [image:303124](#) *clone identifier*
- o [chromosome: 22](#), [locus: 20p*](#), [locus: 7p13](#)

- Search UDB integrated map

specify chromosome:

For example, a map region in [chromosome 19](#).

- Search UDB by gene/marker name

For example, Information about the mapped marker [D17S1843](#).

- View estimated boundaries (in Megabases) of cytogenetic bands

specify chromosome:

What's special about GeneCards?

The information presented here has been **automatically extracted** from various resources by scripts developed in our group. GeneCards is

particularly useful for people who wish to find information about genes of interest in the context of functional genomics and proteomics.

This resource also features a new type of **navigation support** system that **guides** its users to the information. Important parts of this guidance system are the **spell corrector**, and the automatically generated tips for query reformulation.

Developed at the Crown Human Genome Center & Bioinformatics Unit, at the Weizmann Institute of Science

Credits:

Michael Rebhan, Avital Adato, Vered Chalifa-Caspi, Inga Peter, Jaime Prilusky,
Michal Ronen, Hershel Safer, Marilyn Safran, Shai Shen-Orr, Liora Yaar,
Doron Lancet

Comments to: cards@bioinfo.weizmann.ac.il

** Entries with HUGO-approved symbols.*

[Back to top](#)